

R. Hayes

10/24
HSRAW SEQUENCE LISTING
PATENT APPLICATION US/09/170,042DATE: 03/17/2000
TIME: 11:30:50

INPUT SET: S35072.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: HASTINGS, GREGG,
6 PATRICK J. DILLON
7
8 (ii) TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
9
10 (iii) NUMBER OF SEQUENCES: 18
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
14 (B) STREET: 9410 KEY WEST AVENUE
15 (C) CITY: ROCKVILLE
16 (D) STATE: MD
17 (E) COUNTRY: USA
18 (F) ZIP: 20850
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/170,042
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US/08/799,173
33 (B) FILING DATE: 11-FEB-1997
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: BROOKES, ANDERS A.
37 (B) REGISTRATION NUMBER: 36,373
38 (C) REFERENCE/DOCKET NUMBER: PF226
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (301) 309-8504
42 (B) TELEFAX: (301) 309-8512
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

ENTERED

TC 100
MAR 22 2000
RECEIVED
MAIL ROOM

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/170,042DATE: 03/17/2000
TIME: 11:30:50

INPUT SET: S35072.raw

47 (A) LENGTH: 1105 base pairs
 48 (B) TYPE: nucleic acid
 49 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

51 (ii) MOLECULE TYPE: DNA (genomic)
 52

53
 54 (ix) FEATURE:
 55 (A) NAME/KEY: CDS
 56 (B) LOCATION: 19..1011

57
 58 (ix) FEATURE:
 59 (A) NAME/KEY: mat_peptide
 60 (B) LOCATION: 19..963

61

62
 63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 64

65 CGCTGCTCCT GCCGGGTG ATG GAA AAC CCC AGC CCG GCC GCC CTG GGC 51
 66 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly
 67 1 5 10
 68
 69 AAG GCC CTC TGC GCT CTC CTG GCC ACT CTC GGC GCC GCC GGC CAG 99
 70 Lys Ala Leu Cys Ala Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln
 71 15 20 25
 72
 73 CCT CTT GGG GGA GAG TCC ATC TGT TCC GCC AGA GCC CTG GCC AAA TAC 147
 74 Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr
 75 30 35 40
 76
 77 AGC ATC ACC TTC ACG GGC AAG TGG AGC CAG ACG GCC TTC CCC AAG CAG 195
 78 Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln
 79 45 50 55
 80
 81 TAC CCC CTG TTC CGC CCC CCT GCC CAG TGG TCT TCG CTG CTG GGG GCC 243
 82 Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 83 60 65 70 75
 84
 85 GCG CAT AGC TCC GAC TAC AGC ATG TGG AGG AAG AAC CAG TAC GTC AGT 291
 86 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser
 87 80 85 90
 88
 89 AAC GGG CTG CGC GAC TTT GCG GAG CGC GGC GAG GCC TGG GCG CTG ATG 339
 90 Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met
 91 95 100 105
 92
 93 AAG GAG ATC GAG GCG GCG GGG GAG GCG CTG CAG AGC GTG CAC GCG GTG 387
 94 Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val
 95 110 115 120
 96
 97 TTT TCG GCG CCC GCC GTC CCC AGC GGC ACC GGG CAG ACG TCG GCG GAG 435
 98 Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu
 99

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TC 1600 MAIL ROOM

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/170,042DATE: 03/17/2000
TIME: 11:30:51

INPUT SET: S35072.raw

| | | | | |
|-----|---|-----|-----|------|
| 100 | 125 | 130 | 135 | |
| 101 | CTG GAG GTG CAG CGC AGG CAC TCG CTG GTC TCG TTT GTG GTG CGC ATC | | | 483 |
| 102 | Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile | | | |
| 103 | 140 | 145 | 150 | 155 |
| 104 | | | | |
| 105 | GTG CCC AGC CCC GAC TGG TTC GTG GGC GTG GAC AGC CTG GAC CTG TGC | | | 531 |
| 106 | Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys | | | |
| 107 | 160 | 165 | 170 | |
| 108 | | | | |
| 109 | GAC GGG GAC CGT TGG CGG GAA CAG GCG GCG CTG GAC CTG TAC CCC TAC | | | 579 |
| 110 | Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr | | | |
| 111 | 175 | 180 | 185 | |
| 112 | | | | |
| 113 | GAC GCC GGG ACG GAC AGC GGC TTC ACC TTC TCC TCC CCC AAC TTC GCC | | | 627 |
| 114 | Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala | | | |
| 115 | 190 | 195 | 200 | |
| 116 | | | | |
| 117 | ACC ATC CCG CAG GAC ACG GTG ACC GAG ATA ACG TCC TCC TCT CCC AGC | | | 675 |
| 118 | Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser | | | |
| 119 | 205 | 210 | 215 | |
| 120 | | | | |
| 121 | CAC CCG GCC AAC TCC TTC TAC TAC CCG CGG CTG AAG GCC CTG CCT CCC | | | 723 |
| 122 | His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro | | | |
| 123 | 220 | 225 | 230 | 235 |
| 124 | | | | |
| 125 | ATC GCC AGG GTG ACA CTG GTG CGG CTG CGA CAG AGC CCC AGG GCC TTC | | | 771 |
| 126 | Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe | | | |
| 127 | 240 | 245 | 250 | |
| 128 | | | | |
| 129 | ATC CCT CCC GCC CCA GTC CTG CCC AGC AGG GAC AAT GAG ATT GTA GAC | | | 819 |
| 130 | Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp | | | |
| 131 | 255 | 260 | 265 | |
| 132 | | | | |
| 133 | AGC GCC TCA GTT CCA GAA ACG CCG CTG GAC TGC GAG GTC TCC CTG TGG | | | 867 |
| 134 | Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp | | | |
| 135 | 270 | 275 | 280 | |
| 136 | | | | |
| 137 | TCG TCC TGG GGA CTG TGC GGA GGC CAC TGT GGG AGG CTC GGG ACC AAG | | | 915 |
| 138 | Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys | | | |
| 139 | 285 | 290 | 295 | |
| 140 | | | | |
| 141 | AGC AGG ACT CGC TAC GTC CGG GTC CAG CCC GCC AAC AAC GGG AGC CCC | | | 963 |
| 142 | Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro | | | |
| 143 | 300 | 305 | 310 | 315 |
| 144 | | | | |
| 145 | TGC CCC GAG CTC GAA GAA GAG GCT GAG TGC GTC CCT GAT AAC TGC GTC | | | 1011 |
| 146 | Cys Pro Glu Leu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val | | | |
| 147 | 320 | 325 | 330 | |
| 148 | | | | |
| 149 | TAAGACCAGA GCCCCGCAGC CCCTGGGGCC CCCCGGAGCC ATGGGGTGTGTC GGGGGCTCCT | | | 1071 |
| 150 | | | | |
| 151 | GTGCAGGCTC ATGCTGCAGG CGGCCGAGGG CACA | | | 1105 |
| 152 | | | | |

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153

154

155 (2) INFORMATION FOR SEQ ID NO:2:

156

157

(i) SEQUENCE CHARACTERISTICS:

158

(A) LENGTH: 331 amino acids

159

(B) TYPE: amino acid

160

(D) TOPOLOGY: linear

161

162

(ii) MOLECULE TYPE: protein

163

164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

165

Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
166 1 5 10 15

167

Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
168 20 25 30
169

170

Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr Ser Ile Thr Phe Thr
171 35 40 45
172

173

Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
174 50 55 60
175

176

Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
177 65 70 75 80
178

179

Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
180 85 90 95
181

182

Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
183 100 105 110
184

185

Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
186 115 120 125
187

188

Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
189 130 135 140
190

191

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
192 145 150 155 160
193

194

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
195 165 170 175
196

197

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
198 180 185 190
199

200

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
201 195 200 205
202

203

Thr Val Thr Glu Ile Thr Ser Ser Pro Ser His Pro Ala Asn Ser
204 205

205

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206 210 215 220
207 Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
208 225 230 235 240
210 Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
211 245 250 255
212
213 Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
214 260 265 270
215
216 Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
217 275 280 285
218
219 Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
220 290 295 300
221
222 Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu
223 305 310 315 320
224
225 Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
226 325 330
227
228 (2) INFORMATION FOR SEQ ID NO:3:
229
230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 36 base pairs
232 (B) TYPE: nucleic acid
233 (C) STRANDEDNESS: single
234 (D) TOPOLOGY: linear
235
236 (ii) MOLECULE TYPE: DNA (genomic)
237
238
239
240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
241
242
243 GCCATACGGG ATCCCCAGCC TCTTGGGGGA GAGTCC
244
245 (2) INFORMATION FOR SEQ ID NO:4:
246
247 (i) SEQUENCE CHARACTERISTICS:
248 (A) LENGTH: 35 base pairs
249 (B) TYPE: nucleic acid
250 (C) STRANDEDNESS: single
251 (D) TOPOLOGY: linear
252
253 (ii) MOLECULE TYPE: DNA (genomic)
254
255
256
257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
258

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/170,042**

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Original Text